IN THE CLAIMS:

Please amend the claims as follows.

Claims 1-34. (Cancelled)

35. (Previously presented) A method to detect expression of a first transgenic nucleic acid molecule in a sample having either (a) a detectable amount of mRNA transcribed from a second transgenic nucleic acid molecule or (b) a substantially non-detectable amount of said mRNA, said method comprising providing a complementary DNA of the mRNA, amplifying said complementary DNA and hybridizing said complementary DNA with at least one oligonucleotide designed to hybridize to said second transgenic nucleic acid molecule whereby said hybridizing indicates the expression of said first transgenic nucleic acid molecule in a sample.

36. (Previously presented) A method according to claim 35 further comprising quantitation of mRNA transcribed from said second transgenic nucleic acid molecule.

37. (Previously presented) A method according to claim 35 wherein said second transgenic nucleic acid molecule which is selected from the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences.

38. (Previously presented) A method according to claim 35 wherein said second transgenic nucleic acid molecule is a 3' untranslated sequence from the 3' end of the *Pisum sativum* rbcS E9 gene.

39. (Previously presented) A method according to claim 35 wherein said second transgenic nucleic acid molecule has a sequence of SEQ ID NO: 2.

40. (Previously presented) A method according to claim 35 wherein the at least one oligonucleotide is a sequence which is a molecule selected from the group consisting of SEQ ID NO: 7 SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 28.

41. (Previously presented) A method according to claim 35 wherein the amplifying is carried out by a method selected from the group consisting of PCR or RT-PCR.

42. (Previously presented) A method according to claim 36 wherein the quantitation of mRNA is determined by a method selected from the group consisting of quantitative RT-PCR or competitive quantitative RT-PCR.

43. (Previously presented) A method according to claim 35 wherein said second transgenic nucleic acid molecule comprises at least 100 base pairs of consecutive sequence having a sequence of SEQ ID NO: 2.

44. (Previously presented) A method according to claim 35 wherein at least one oligonucleotide comprises at least 15 bases from or complementary to a consecutive sequence of SEQ ID NO: 2.

45. (Previously presented) A method according to claim 35 wherein at least one oligonucleotide has a detectable label.

46. (Previously presented) A method according to claim 45 wherein said label is selected from the group consisting of a fluorescent label, a digoxigenen-dUTP label, a biotin label, and a radiolabel.

47. (Previously presented) A method according to claim 35 wherein said at least one oligonucleotide comprises a pair of oligonucleotide primers and an oligonucleotide probe designed to hybridize to said second transgenic nucleic acid molecule in a 5' nuclease assay.

48. (Previously presented) A method according to claim 47 wherein each of said primer pair used in said amplification comprises 15 to 30 bases identical or complementary to a consecutive sequence of a second transgenic nucleic acid molecule having a sequence selected from the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences and wherein said probe comprises 15 to 30 bases complementary or

identical to a second transgenic nucleic acid molecule having a sequence selected from the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences.

49. (Previously presented) A method according to claim 35 further comprising Southern Blotting, Northern Blotting or RNAse protection assay.

50. (Currently amended) An amplification kit for the detection of a transgenic nucleic acid molecule comprising at least one primer pair and a corresponding labeled probe which hybridizes under stringent hybridization conditions to a nucleic acid molecule of a 3' untranslated sequence of a 3' end of the *Pisum sativum* rbcS E9 gene.

51. (New) A method to detect expression of a first transgenic nucleic acid molecule in a sample having either (a) a detectable amount of mRNA transcribed from a second transgenic nucleic acid molecule or (b) a substantially non-detectable amount of said mRNA, said method comprising providing a complementary DNA of the mRNA, amplifying said complementary DNA and hybridizing said complementary DNA with at least one oligonucleotide designed to hybridize to said second transgenic nucleic acid molecule whereby said hybridizing indicates the expression of said first transgenic nucleic acid molecule in a sample and wherein said at least one oligonucleotide is a sequence which is a molecule selected from the group consisting of SEQ ID NO: 7 SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 28.

52. (New) A method to detect expression of a first transgenic nucleic acid molecule in a sample having either (a) a detectable amount of mRNA transcribed from a second transgenic nucleic acid molecule or (b) a substantially non-detectable amount of said mRNA, said method comprising providing a complementary DNA of the mRNA, amplifying said complementary DNA and hybridizing said complementary DNA with at least one oligonucleotide designed to hybridize to said second transgenic nucleic acid molecule whereby said hybridizing indicates the expression of said first transgenic nucleic acid molecule in a sample and wherein said second transgenic nucleic acid molecule is the sequence of SEQ ID NO: 2.